



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/502,279

DATE: 07/30/2004

TIME: 09:32:53

Input Set : A:\Q82704 Sequence Listing.txt

Output Set: N:\CRF4\07302004\J502279.raw

3 <110> APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.
4 Hideki ENDOH
5 Ryosuke NAKANO
6 Eiji KUROSAKI
7 Miyuki KATO
8 Hiroyuki YOKOTA
9 Kazunori INABE
11 <120> TITLE OF INVENTION: METHOD FOR SCREENING A DRUG AMELIORATING INSULIN RESISTANCE
13 <130> FILE REFERENCE: Q82704
C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/502,279
C--> 15 <141> CURRENT FILING DATE: 2004-07-23
15 <150> PRIOR APPLICATION NUMBER: JP 2002-013721
16 <151> PRIOR FILING DATE: 2002-01-23
18 <150> PRIOR APPLICATION NUMBER: JP 2002-257703
19 <151> PRIOR FILING DATE: 2002-09-03
21 <160> NUMBER OF SEQ ID NOS: 28
23 <170> SOFTWARE: PatentIn version 3.1
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1518
27 <212> TYPE: DNA
28 <213> ORGANISM: Homo sapiens
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)..(1518)
33 <223> OTHER INFORMATION:

A rectangular stamp with a double-line border. The word "ENTERED" is printed in large, bold, capital letters in the center.



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37 atg ggt gaa act ctg gga gat tct cct att gac cca gaa agc gat tcc      48
38 Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser
39 1           5           10           15
41 ttc act gat aca ctg tct gca aac ata tca caa gaa atg acc atg gtt      96
42 Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val
43           20           25           30
45 gac aca gag atg cca ttc tgg ccc acc aac ttt ggg atc agc tcc gtg      144
46 Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val
47           35           40           45
49 gat ctc tcc gta atg gaa gac cac tcc cac tcc ttt gat atc aag ccc      192
50 Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro
51           50           55           60
53 ttc act act gtt gac ttc tcc agc att tct act cca cat tac gaa gac      240
54 Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp
55 65           70           75           80
57 att cca ttc aca aga aca gat cca gtg gtt gca gat tac aag tat gac      288
58 Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp

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59	85	90	95	
61	ctg aaa ctt caa gag tac caa agt gca atc aaa gtg gag cct gca tct			336
62	Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser			
63	100	105	110	
65	cca cct tat tat tct gag aag act cag ctc tac aat aag cct cat gaa			384
66	Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu			
67	115	120	125	
69	gag cct tcc aac tcc ctc atg gca att gaa tgt cgt gtc tgt gga gat			432
70	Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp			
71	130	135	140	
73	aaa gct tct gga ttt cac tat gga gtt cat gct tgt gaa gga tgc aag			480
74	Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys			
75	145	150	155	160
77	ggt ttc ttc cgg aga aca atc aga ttg aag ctt atc tat gac aga tgt			528
78	Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys			
79	165	170	175	
81	gat ctt aac tgt cgg atc cac aaa aaa agt aga aat aaa tgt cag tac			576
82	Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr			
83	180	185	190	
85	tgt cgg ttt cag aaa tgc ctt gca gtg ggg atg tct cat aat gcc atc			624
86	Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile			
87	195	200	205	
89	agg ttt ggg cgg atg cca cag gcc gag aag gag aag ctg ttg gcg gag			672
90	Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu			
91	210	215	220	
93	atc tcc agt gat atc gac cag ctg aat cca gag tcc gct gac ctc cgg			720
94	Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg			
95	225	230	235	240
97	gcc ctg gca aaa cat ttg tat gac tca tac ata aag tcc ttc ccg ctg			768
98	Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu			
99	245	250	255	
101	acc aaa gca aag gcg agg gcg atc ttg aca gga aag aca aca gac aaa			816
102	Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Asp Lys			
103	260	265	270	
105	tca cca ttc gtt atc tat gac atg aat tcc tta atg atg gga gaa gat			864
106	Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp			
107	275	280	285	
109	aaa atc aag ttc aaa cac atc acc ccc ctg cag gag cag agc aaa gag			912
110	Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu			
111	290	295	300	
113	gtg gcc atc cgc atc ttt cag ggc tgc cag ttt cgc tcc gtg gag gct			960
114	Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala			
115	305	310	315	320
117	gtg cag gag atc aca gag tat gcc aaa agc att cct ggt ttt gta aat			1008
118	Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn			
119	325	330	335	
121	ctt gac ttg aac gac caa gta act ctc ctc aaa tat gga gtc cac gag			1056
122	Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu			
123	340	345	350	

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125 atc att tac aca atg ctg gcc tcc ttg atg aat aaa gat ggg gtt ctc	1104
126 Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu	
127 355 360 365	
129 ata tcc gag ggc caa ggc ttc atg aca agg gag ttt cta aag agc ctg	1152
130 Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu	
131 370 375 380	
133 cga aag cct ttt ggt gac ttt atg gag ccc aag ttt gag ttt gct gtg	1200
134 Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val	
135 385 390 395 400	
137 aag ttc aat gca ctg gaa tta gat gac agc gac ttg gca ata ttt att	1248
138 Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile	
139 405 410 415	
141 gct gtc att att ctc agt gga gac cgc cca ggt ttg ctg aat gtg aag	1296
142 Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys	
143 420 425 430	
145 ccc att gaa gac att caa gac aac ctg cta caa gcc ctg gag ctc cag	1344
146 Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln	
147 435 440 445	
149 ctg aag ctg aac cac cct gag tcc tca cag ctg ttt gcc aag ctg ctc	1392
150 Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu	
151 450 455 460	
153 cag aaa atg aca gac ctc aga cag att gtc acg gaa cac gtg cag cta	1440
154 Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu	
155 465 470 475 480	
157 ctg cag gtg atc aag aag acg gag aca gac atg agt ctt cac ccg ctc	1488
158 Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu	
159 485 490 495	
161 ctg cag gag atc tac aag gac ttg tac tag	1518
162 Leu Gln Glu Ile Tyr Lys Asp Leu Tyr	
163 500 505	
166 <210> SEQ ID NO: 2	
167 <211> LENGTH: 505	
168 <212> TYPE: PRT	
169 <213> ORGANISM: Homo sapiens	
171 <400> SEQUENCE: 2	
173 Met Gly Glu Thr Leu Gly Asp Ser Pro Ile Asp Pro Glu Ser Asp Ser	
174 1 5 10 15	
177 Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Met Thr Met Val	
178 20 25 30	
181 Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val	
182 35 40 45	
185 Asp Leu Ser Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro	
186 50 55 60	
189 Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp	
190 65 70 75 80	
193 Ile Pro Phe Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp	
194 85 90 95	
197 Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser	
198 100 105 110	

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201 Pro Pro Tyr Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu
202 115 120 125
205 Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp
206 130 135 140
209 Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys
210 145 150 155 160
213 Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys
214 165 170 175
217 Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr
218 180 185 190
221 Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn Ala Ile
222 195 200 205
225 Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu Ala Glu
226 210 215 220
229 Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp Leu Arg
230 225 230 235 240
233 Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe Pro Leu
234 245 250 255
237 Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr Asp Lys
238 260 265 270
241 Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu Asp
242 275 280 285
245 Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser Lys Glu
246 290 295 300
249 Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu Ala
250 305 310 315 320
253 Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val Asn
254 325 330 335
257 Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu
258 340 345 350
261 Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val Leu
262 355 360 365
265 Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser Leu
266 370 375 380
269 Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala Val
270 385 390 395 400
273 Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe Ile
274 405 410 415
277 Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn Val Lys
278 420 425 430
281 Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu Gln
282 435 440 445
285 Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu Leu
286 450 455 460
289 Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln Leu
290 465 470 475 480
293 Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro Leu
294 485 490 495
297 Leu Gln Glu Ile Tyr Lys Asp Leu Tyr

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Input Set : A:\Q82704 Sequence Listing.txt
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298	500	505	
301 <210> SEQ ID NO: 3			
302 <211> LENGTH: 987			
303 <212> TYPE: DNA			
304 <213> ORGANISM: Homo sapiens			
306 <220> FEATURE:			
307 <221> NAME/KEY: CDS			
308 <222> LOCATION: (1)..(987)			
309 <223> OTHER INFORMATION:			
W--> 311 <400> 3			
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313 Met Ala Ala Gly Ile Val Ala Ser Arg Arg Leu Arg Asp Leu Leu Thr			
314 1 5 10 15			
316 cgg cga ctg aca ggc tcc aac tac ccg gga ctc agt att agc ctt cgc			96
317 Arg Arg Leu Thr Gly Ser Asn Tyr Pro Gly Leu Ser Ile Ser Leu Arg			
318 20 25 30			
320 ctc act ggc tcc tct gca caa gag gcg gct tcc gga gta gcc ctc ggt			144
321 Leu Thr Gly Ser Ser Ala Gln Glu Ala Ala Ser Gly Val Ala Leu Gly			
322 35 40 45			
324 gaa gcc cca gac cac agc tat gag tcc ctt cgt gtg acg tct gcg cag			192
325 Glu Ala Pro Asp His Ser Tyr Glu Ser Leu Arg Val Thr Ser Ala Gln			
326 50 55 60			
328 aaa cat gtt ctg cat gtc cag ctc aac ccg ccc aac aag agg aat gcc			240
329 Lys His Val Leu His Val Gln Leu Asn Arg Pro Asn Lys Arg Asn Ala			
330 65 70 75 80			
332 atg aac aag gtc ttc tgg aga gag atg gta gag tgc ttc aac aag att			288
333 Met Asn Lys Val Phe Trp Arg Glu Met Val Glu Cys Phe Asn Lys Ile			
334 85 90 95			
336 tcg aga gac gct gac tgt ccg gcg gtg atc tct ggt gca gga aaa			336
337 Ser Arg Asp Ala Asp Cys Arg Ala Val Val Ile Ser Gly Ala Gly Lys			
338 100 105 110			
340 atg ttc act gca ggt att gac ctg atg gac atg gct tcg gac atc ctg			384
341 Met Phe Thr Ala Gly Ile Asp Leu Met Asp Met Ala Ser Asp Ile Leu			
342 115 120 125			
344 cag ccc aaa gga gat gat gtg gcc ccg atc agc tgg tac ctc cgt gac			432
345 Gln Pro Lys Gly Asp Asp Val Ala Arg Ile Ser Trp Tyr Leu Arg Asp			
346 130 135 140			
348 atc atc act cga tac cag gag acc ttc aac gtc atc gag agg tgc ccc			480
349 Ile Ile Thr Arg Tyr Gln Glu Thr Phe Asn Val Ile Glu Arg Cys Pro			
350 145 150 155 160			
352 aag ccc gtg att gct gcc gtc cat ggg ggc tgc att ggc gga ggt gtg			528
353 Lys Pro Val Ile Ala Ala Val His Gly Gly Cys Ile Gly Gly Val			
354 165 170 175			
356 gac ctt gtc acc gcc tgt gac atc ccg tac tgt gcc cag gat gct ttc			576
357 Asp Leu Val Thr Ala Cys Asp Ile Arg Tyr Cys Ala Gln Asp Ala Phe			
358 180 185 190			
360 ttc cag gtg aag gag gtg gac gtg ggt ttg gct gcc gat gta gga aca			624.
361 Phe Gln Val Lys Glu Val Asp Val Gly Leu Ala Ala Asp Val Gly Thr			
362 195 200 205			

VERIFICATION SUMMARY

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Input Set : A:\Q82704 Sequence Listing.txt
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L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:36 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:33
L:311 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:309
L:498 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:496
L:757 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:755
L:970 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:16,Line#:968
L:1219 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:1217